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OM protein - protein search, using sw model

Run on: July 28, 2004, 11:26:10 ; Search time 14 Seconds
(without alignments)
799.649 Million cell updates/sec

Title: US-10-028-072-4
Perfect score: 1132
Sequence: 1 MVSMFKNRSDRYSTRCC.....PEIAVYPAFESTSVRFANL 215

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|--------------|---------------------|
| 1 | 1087 | 96.0 | 233 | 1 MTRP_HUMAN | Q15012 homo sapien |
| 2 | 1061 | 93.7 | 233 | 1 MTRP_MOUSE | Q60961 mus musculus |
| 3 | 191 | 16.9 | 262 | 1 LAM5_HUMAN | Q13571 homo sapien |
| 4 | 189.5 | 16.7 | 261 | 1 LAM5_MOUSE | Q61168 mus musculus |
| 5 | 103.5 | 9.1 | 385 | 1 G22C_DROME | P58952 drosophila |
| 6 | 93 | 8.2 | 413 | 1 Y567_BUCAP | Q8k902 buchnera ap |
| 7 | 90 | 8.0 | 274 | 1 NU2M_DROME | P29867 drosophila |
| 8 | 89.5 | 7.9 | 446 | 1 D3DR_MOUSE | P30728 mus musculus |
| 9 | 89.5 | 7.9 | 446 | 1 D3DR_RAT | P19020 rattus norv |
| 10 | 88 | 7.8 | 551 | 1 FIXN_AZOCA | P98056 azorhizobiu |
| 11 | 87.5 | 7.7 | 432 | 1 Y672_METJA | Q58086 methanococc |
| 12 | 87.5 | 7.7 | 535 | 1 YDW6_SCHPO | Q13912 schizosacch |
| 13 | 87 | 7.7 | 341 | 1 NU2M_DROME | P03896 drosophila |
| 14 | 87 | 7.7 | 2253 | 1 PKDR_HUMAN | Q9ntg1 homo sapien |
| 15 | 86.5 | 7.6 | 112 | 1 YUW4_CAEEL | Q20263 caenorhabdi |
| 16 | 86.5 | 7.6 | 1163 | 1 KCH2_RAT | O08962 rattus norv |
| 17 | 85.5 | 7.6 | 341 | 1 NU2M_DROYA | P03895 drosophila |
| 18 | 85.5 | 7.6 | 379 | 1 CYB_TRASR | Q9t9b7 tragelaphus |
| 19 | 85.5 | 7.6 | 457 | 1 YG90_HAEIN | P45320 haemophilus |
| 20 | 85.5 | 7.6 | 570 | 1 NUSM_PARTE | P15584 paramecium |
| 21 | 85 | 7.5 | 379 | 1 CYB_CAMBA | Q34028 camelus bac |
| 22 | 85 | 7.5 | 695 | 1 CIO4_HUMAN | P56696 homo sapien |
| 23 | 84.5 | 7.5 | 267 | 1 CYB_AKOCU | P48518 akodon curs |
| 24 | 84.5 | 7.5 | 379 | 1 CYB_FERAT | Q9tdn1 feresa atte |
| 25 | 84.5 | 7.5 | 379 | 1 CYB_KOBEL | O99342 kobus ellip |
| 26 | 84.5 | 7.5 | 379 | 1 CYB_MUNMU | Q9tdq7 muntiacus m |
| 27 | 84.5 | 7.5 | 379 | 1 CYB_ZIPCA | Q36262 ziphius cav |
| 28 | 84.5 | 7.5 | 590 | 1 NUSM_TRYBB | P04540 trypanosoma |
| 29 | 84.5 | 7.5 | 1159 | 1 KCH2_HUMAN | Q12809 homo sapien |
| 30 | 84.5 | 7.5 | 1162 | 1 KCH2_MOUSE | Q35219 mus musculus |
| 31 | 84 | 7.4 | 379 | 1 CYB_VESMU | Q957c8 vespertilio |
| 32 | 83.5 | 7.4 | 379 | 1 CYB_BUBBU | Q33950 bubalus bub |
| 33 | 83.5 | 7.4 | 379 | 1 CYB_BUEDE | P92870 bubalus dep |

| | | | | | | |
|----|------|-----|-----|---|------------|---------------------|
| 34 | 83.5 | 7.4 | 379 | 1 | CYB_BUBQU | P92592 bubalus qua |
| 35 | 83.5 | 7.4 | 379 | 1 | CYB_MYONA | Q95629 myotis natt |
| 36 | 83.5 | 7.4 | 423 | 1 | GP83_MOUSE | P30731 mus musculus |
| 37 | 83 | 7.3 | 379 | 1 | CYB_FTEHP | Q8sjz4 pteropus hy |
| 38 | 83 | 7.3 | 470 | 1 | MTR_NEUCR | P38680 neurospora |
| 39 | 83 | 7.3 | 783 | 1 | YAF3_YEAST | P39719 saccharomyc |
| 40 | 82.5 | 7.3 | 274 | 1 | NU2M_DROSE | P29868 drosophila |
| 41 | 82.5 | 7.3 | 274 | 1 | NU2M_DROSI | P29869 drosophila |
| 42 | 82.5 | 7.3 | 380 | 1 | CYB_APOSE | Q9t9i7 apogon semi |
| 43 | 82.5 | 7.3 | 380 | 1 | CYB_NEORH | Q8h1b9 neocytus r |
| 44 | 82.5 | 7.3 | 380 | 1 | CYB_POLOR | Q95920 polypterus |
| 45 | 82 | 7.2 | 300 | 1 | NU2M_ASCSU | P24877 ascaris suu |

ALIGNMENTS

RESULT 1
MTRP_HUMAN
ID MTRP_HUMAN STANDARD; PRT; 233 AA.
AC Q15012;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lysosomal-associated transmembrane protein 4A (Golgi 4-transmembrane
DE spanning transporter MTP)
GN LAPTMA4 OR MTRP OR KIAA0108.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=95308325; PubMed=7788527;
RA Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S.,
RA Tabata S., Ishikawa K.-I., Kawarabayashi Y., Kotani H., Nomura N.,
RA "Prediction of the coding sequences of unidentified human genes. III.
RA The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by
RA analysis of cDNA clones from human cell line KG-1."
RL DNA Res. 2:37-43(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Jones S.J.M., Marra M.A.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May function in the transport of nucleosides and/or
CC nucleoside derivatives between the cytosol and the lumen of an
CC intracellular membrane-bound compartment (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. May reside in an
CC intracellular membrane-bound compartment (Potential).
CC -!- DOMAIN: The C-terminal domain is necessary for retention within
CC intracellular membranes (By similarity).
CC -----

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CC -----

DR EMBL; D14696; BAA03522.1; --
DR EMBL; BC000421; AAH00421.1; --
DR Genew; HGNC:6924; LAPTM4A.
DR InterPro; IPR004687; Mtp.
DR Pfam; PF03821; Mtp; 1.
DR TIGRFAMs; TIGR00799; mtp; 1.
KW Transmembrane; Transport.
FT TRANSMEM 29 49 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 108 128 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
FT DOMAIN 226 229 POLY-PRO.
SQ SEQUENCE 233 AA; 26800 MW; 9BB76152B6E1365E CRC64;

Query Match 96.0%; Score 1087; DB 1; Length 233;
Best Local Similarity 99.5%; Pred. No. 1.6e-78;
Matches 205; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSMSPKRNRSDFYSTRCCGCHVTRGTIIIGTWYVNVLLMAILLTVEVTHPNSMPAV 60
Db 1 MVSMSPKRNRSDFYSTRCCGCHVTRGTIIIGTWYVNVLLMAILLTVEVTHPNSMPAV 60
QY 61 NQYEVIGNYSSERMADNACVLFVAVSVLMFISSMLVYGAIQVGVGLIPFFCYRLDF 120
Db 61 NQYEVIGNYSSERMADNACVLFVAVSVLMFISSMLVYGAIQVGVGLIPFFCYRLDF 120
QY 121 VLSCLVAISSLTYPRIKEYLDQLDPFPYKDDLLALDSSCLLFVIVLFFKAYLI 180
Db 121 VLSCLVAISSLTYPRIKEYLDQLDPFPYKDDLLALDSSCLLFVIVLFFKAYLI 180
QY 181 NCVWNCYKYNRNVPPIAVYPAFES 206
Db 181 NCVWNCYKYNRNVPPIAVYPAFEA 206

RESULT 2

MTRP MOUSE
ID MTRP MOUSE STANDARD; PRT; 233 AA.
AC Q60961;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lysosomal-associated transmembrane protein 4A (Golgi 4-transmembrane
DE spanning transporter) (Mouse transporter protein) (MTP).
GN LAPTM4A OR MTRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2; TISSUE=Brain, and Leukemia;
RX MEDLINE=96199248; PubMed=8621662;
RA Hogue D.L., Ellison M.J., Young J.D., Cass C.E.;
RT "Identification of a novel membrane transporter associated with
RT intracellular membranes by phenotypic complementation in the yeast
RT Saccharomyces cerevisiae";
RL J. Biol. Chem. 271:9801-9808(1996).
CC -1- FUNCTION: May function in the transport of nucleosides and/or
CC nucleoside derivatives between the cytosol and the lumen of an
CC intracellular membrane-bound compartment.
CC -2- SUBCELLULAR LOCATION: Integral membrane protein. May reside in an
CC intracellular membrane-bound compartment (Potential). Isoform
CC probably be localized in the plasma membrane.

CC Event=Alternative initiation;
CC Comment=2 isoforms, long (shown here) and Short/Truncated/MTP1,
CC may be produced by alternative initiation;
CC -1- DOMAIN: The C-terminal domain is necessary for retention within
CC intracellular membranes.
CC -----

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DR EMBL; U34259; AAB04938.1; --
DR MGI; MGI:108017; Laptm4a.
DR InterPro; IPR004687; Mtp.
DR Pfam; PF03821; Mtp; 1.
DR TIGRFAMs; TIGR00799; mtp; 1.
KW Transmembrane; Transport; Alternative initiation.
FT CHAIN 1 233 LYSOSOMAL-ASSOCIATED TRANSMEMBRANE
FT CHAIN 90 233 PROTEIN 4A, ISOFORM LONG.
FT INIT MET 90 90 LYSOSOMAL-ASSOCIATED TRANSMEMBRANE
FT TRANSMEM 29 49 PROTEIN 4A, ISOFORM SHORT.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 108 128 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
FT DOMAIN 226 229 POLY-PRO.
SQ SEQUENCE 233 AA; 26857 MW; CA409AC77ACE4D6E CRC64;

Query Match 93.7%; Score 1061; DB 1; Length 233;
Best Local Similarity 97.1%; Pred. No. 1.7e-76;
Matches 200; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVSMSPKRNRSDFYSTRCCGCHVTRGTIIIGTWYVNVLLMAILLTVEVTHPNSMPAV 60
Db 1 MVSMSPKRNRSDFYSTRCCGCHVTRGTIIIGTWYVNVLLMAILLTVEVTHPNSMPAV 60
QY 61 NQYEVIGNYSSERMADNACVLFVAVSVLMFISSMLVYGAIQVGVGLIPFFCYRLDF 120
Db 61 NQYEVIGNYSSERMADNACVLFVAVSVLMFISSMLVYGAIQVGVGLIPFFCYRLDF 120
QY 121 VLSCLVAISSLTYPRIKEYLDQLDPFPYKDDLLALDSSCLLFVIVLFFKAYLI 180
Db 121 VLSCLVAISSLTYPRIKEYLDQLDPFPYKDDLLALDSSCLLFVIVLFFKAYLI 180
QY 181 NCVWNCYKYNRNVPPIAVYPAFES 206
Db 181 NCVWNCYKYNRNVPPIAVYPAFET 206

RESULT 3

LAM5_HUMAN
ID LAM5_HUMAN STANDARD; PRT; 262 AA.
AC Q13571; Q13240; Q14698;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysosomal-associated multitransmembrane protein (Retinoic acid-
DE inducible E3 protein) (HA1520).
GN LAPTM5 OR KIAA0085.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=96299782; PubMed=8661146;
RA Adra C.N., Zhu S., Ko J.-L., Guillemot J.-C., Cuervo A.M.,
RA Kobayashi H., Horiuchi T., Lelias J.-M., Rowley J.D., Lim B.;